

RESULT 1

LOCUS HUM1HH 1277 bp mRNA PRI 12-FEB-1995

DEFINITION Homo sapiens Indian hedgehog protein (IHH) mRNA, 5' end.

ACCESSION L38517

VERSION L38517.1 GI:663154

KEYWORDS homologue; Indian hedgehog protein.

SOURCE Homo sapiens (clone HHH4) (tissue library: Clontech) fetus lung

ORGANISM Homo sapiens

CDNA to mRNA.

REFERENCE 1 (bases 1 to 1277)

AUTHORS Marigo, V., Roberts, D.J., Lee, S.M.K., Tsukurov, O., Levi, T., Gaster, J.M., Epstein, D.J., Gilbert, D.J., Martin, G.G., Copeland, N.G., Seidman, C.E., Jenkins, N.A., Seldman, J.G., McMahon, A.P., and Tabin, C.

TITLE Cloning, expression and chromosomal location of SHH and IHH, two human homologues of the Drosophila segment polarity gene Hedgehog

JOURNAL Unpublished (1995)

FEATURES

source

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e-211;

Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 185 AATAGTATGAGCTGCGCGGCTTGAGAGTGAAGCGGCTTGAGCTGGGTGATTTAC 244

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DB 1145 TGAGCTGGGAGGAGTGTGTTGACCCCTCTCTCTAGAGACTTGAAGCTGGACGG 1204

1551 CGACTCCCAACTAGCTGCTCTACAGAGTTTATCTGCTGCTGCTGCTGCTGCTGCTG 1610

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1611 GGGCCATTCCT 1622

DB 1265 GGGCCATTCCT 1276

RESULT 2

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2000, 04:52:15 ; Search time 1833.88 Seconds  
(without alignments)  
-860.399 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	843.2	52.0	1056	5	AR021200
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8	828.6	51.1	1011	12	MMIHR
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10	661.2	40.8	683	9	AB01009253
11	618.8	38.2	1635	4	AF047465
12	509.6	31.4	1230	4	XLU26404
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14	459	28.3	1277	5	AR021198
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#### ALIGNMENTS

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AB010092 Homo sapi  
AF144100 Bos tauru  
S66384 hh-segment

RESULT	1
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DEFINITION	Homo sapiens Indian hedgehog protein (IHH) mRNA, 5' end.
ACCESSION	L38517
VERSION	L38517.1 GI:663154
KEYWORDS	homologue; Indian hedgehog protein.
SOURCE	Homo sapiens (clone HHH4) (tissue library: Clontech) fetus lung cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1277) Matigoe,V., Roberts,D.J., Lee,S.M.K., Tsukurov,O., Levi,T., Gasler,J.W., Epstein,D.J., Gilbert,D.J., Martin,G.G., Copeland,N.G., Seidman,C.E., Jenkins,N.A., Seidman,J.G., McPherson,A.P. and Tadin,C.
TITLE	Cloning, expression and chromosomal location of SHH and IHH, two human homologues of the Drosophila segment polarity gene Hedgehog unpublished (1995)
JOURNAL	Location/Qualifiers
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VERSION	G28584.1	GI:1408399			
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SOURCE	human.				
ORGANISM	Homo sapiens				
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AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
JOURNAL	1 (bases 1 to 1277)				
COMMENT	Myers, R.M.				
	Unpublished (1996)				
	Contact: Richard M. Myers				
	Stanford Human Genome Center (SHGC)				
	Stanford University School of Medicine				
	Department of Genetics, M-344, Stanford, CA 94305, USA				
	Tel: 415/725/9687				
	Fax: 415/725/9689				
	Email: myerseshgc.stanford.edu				
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Qy	1011	TCCTACACAGGGGCGCCGCGGGGCTCAGGCCCGCGCTCACAAACATGGGAGCACTGGTGTG	1070
Db	665	TCCTACACAGGTGGGCTCGCGGGGCTCAGGCCCGCGCTCACAAACATGGGAGCACTGGTGTG	724
Qy	1071	GAGGATGTGTGGATCTGTGCTTCGCGGGCGTGTGGCTGACACACACTGACTCAGTTGGCC	1130
Db	725	GAGGATGTGTGGGATCTGTGCTTCGCGGGCGTGTGGCTGACACACACTGACTCAGTTGGCC	784
Qy	1131	TTCTGGCGCCCTGAGACTCTTTCACACACTTGGCATGGGAGACTGGAACCCCGGGGGAGGCT	1190
Db	785	TTCTGGCGCCCTGAGACTCTTTCACACACTTGGCATGGGAGACTGGAACCCCGGGGGAGGCT	844
Qy	1191	GTCGATTGTGATCCCGGACGCTCTCAACGCGCTGGGGCGCTCCTCTCTGAAAGAGGCGACG	1250
Db	845	GTCGATTGTGATCCCGGACGCTCTCAACGCGCTGGGGCGCTCCTCTCTGAAAGAGGCGACG	904
Qy	1251	TTTCACCCACTGGGATGTCCGGGGGAGGAGCTGAAAGACTCCACGCTGCCCTCTG	1310
Db	905	TTTCACCCACTGGGATGTCCGGGGGAGGAGCTGAAAGACTCCACGCTGCCCTCTG	964
Qy	1311	GACTGCTGTGATGGGTGTCGAGAGCCCTTCACGACGAGAGGAGCTGGCGCTGGAAGGAC	1370
Db	965	GACTGCTGTGATGGGTGTCGAGAGCCCTTCACGACGAGAGGAGCTGGCGCTGGAAGGAC	1024
Qy	1371	CTGAGCTGGGGGACACTGAGCTCTCGCATCTCCTTGCCATCAATACACATTGAGAC	1430
Db	1025	CTGAGCTGGGGGACACTGAGCTCTCGCATCTCCTTGCCATCAATACACATTGAGAC	1084
Qy	1431	TTGACTGGGCAACACAGAGCTCCCCACCGCGCTGTGTGTGATCATTAGAGCTCAAGC	1490
Db	1085	TTGACTGGGCAACACAGAGCTCCCCACCGCGCTGTGTGTGATCATTAGAGCTCAAGC	1144
Qy	1491	TGAGCTGGCGAGGGAGTGTGTGTGACCCCTCTCTCTCTGAAACCTTGGAGCTGGCAGG	1550
Db	1145	TGAGCTGGCGAGGGAGTGTGTGTGACCCCTCTCTCTCTGAAACCTTGGAGCTGGCAGG	1204
Qy	1551	CGACTCCCAACTAGCCTGCTCTCACTACGAGTTTCATTACTGTCTCCCATTTGGGA	1610

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Db 1509 GGGCATGTCTGGGGGAGAGAGCTGAAGAGCTTAACCACTGCTCTCTGGAAGCTCTGT 1568  
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 Db 1569 GGTGATTCAGAGAGAGCTCTCAGCAGAGAGAGAGCTGGCCCTGGAGAGAGAGCTGAG 1628  
 QY 1381 GGAACATGCTCTCTGCT 1440  
 Db 1629 GTTGTCTCCGTC-----CTCTGTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1681  
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RESULT 4  
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 LOCUS AR063086 Sequence 7 from patent US 5844079.  
 DEFINITION AR063086  
 VERSION AR063086.1 GI:5990777  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 939)  
 AUTHORS Ingham, P.W., McMahon, A.P. and Tabin, C.J.  
 TITLE Vertebrate embryonic pattern-inducing proteins, and uses related thereto  
 JOURNAL Patent: US 5844079-A 7 01-DEC-1998;  
 FEATURES Location/Qualifiers  
 source 1..939  
 BASE COUNT 154 a 305 c 314 g 166 t  
 ORIGIN

Query Match 57.7%; Score 936; DB 5; Length 939;

Best Local Similarity 100.0%; Pred. No. 8e-153; Mismatches 0; Indels 0; Gaps 0;

Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 351 CGCCTCATGACCCAGGCTGCAAGAGACCGGCTGACTGCTGCTATCTGCTGATGAAC 410  
 Db 4 CGCCTCATGACCCAGGCTGCAAGAGACCGGCTGACTGCTGCTATCTGCTGATGAAC 63  
 QY 411 CAGTGCCCGGCTGTAAGCTGCGGCTGACCGAGGCTGGAGAGAGAGAGAGAGAGAGAGAG 470  
 Db 64 CAGTGCCCGGCTGTAAGCTGCGGCTGACCGAGGCTGGAGAGAGAGAGAGAGAGAGAGAG 123  
 QY 471 GAGAGATCCCTGATATGAG 530  
 Db 124 GAGAGATCCCTGATATGAG 183  
 QY 531 AATAGATGAG 590  
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 QY 591 GAGTCAAG 650  
 Db 244 GAGTCAAG 303  
 QY 651 GGGGAG 710  
 Db 304 GGGGAG 363  
 QY 711 TCAAGCGTGAAG 770  
 Db 364 TCAAGCGTGAAG 423

QY 771 AGCATGTCTCATTTTCTCTGAG 830  
 Db 424 AGCATGTCTCATTTTCTCTGAG 483  
 QY 831 GAGACTCAG 890  
 Db 484 GAGACTCAG 543  
 QY 891 GACATCAG 950  
 Db 544 GACATCAG 603  
 QY 951 GGCAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010  
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 QY 1011 TCTACAG 1070  
 Db 664 TCTACAG 723  
 QY 1071 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1130  
 Db 724 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783  
 QY 1131 TCTGAG 1190  
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 QY 1191 GTGATGTGTACCCAG 1250  
 Db 844 GTGATGTGTACCCAG 903  
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 Db 904 TTCCACCCAG 939

RESULT 5  
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 AC016762  
 VERSION AC016762.1 GI:6524279  
 KEYWORDS HTG; HTGS\_PBASE1.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 173557)  
 AUTHORS Waterston, R.H.  
 TITLE The sequence of Homo sapiens clone  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 173557)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

## COMMENT

\* NOTE: This is a "working draft" sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
 \* 1 2608: contig of 2608 bp in length  
 \* 2627: gap of unknown length  
 \* 2628 4664: contig of 2037 bp in length  
 \* 4683: gap of unknown length  
 \* 4684 7270: contig of 2367 bp in length

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* 7271 7289: gap of unknown length
* 7290 10058: contig of 2769 bp in length
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* 10078 12127: contig of 2050 bp in length
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* 12147 14784: contig of 2638 bp in length
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* 16982 17000: gap of unknown length
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* 21234 25084: contig of 3851 bp in length
* 25085 25103: gap of unknown length
* 25104 28185: contig of 3082 bp in length
* 28186 28204: gap of unknown length
* 28205 31202: contig of 2998 bp in length
* 31203 31221: gap of unknown length
* 31222 34083: contig of 2862 bp in length
* 34084 34102: gap of unknown length
* 34103 37104: contig of 3002 bp in length
* 37105 37123: gap of unknown length
* 37124 40839: contig of 3716 bp in length
* 40840 40858: gap of unknown length
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* 51460 53846: contig of 2387 bp in length
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* 56897 59964: contig of 3068 bp in length
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* 59984 63028: contig of 3045 bp in length
* 63029 63047: gap of unknown length
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* 66372 70572: contig of 4201 bp in length
* 70573 70592: gap of unknown length
* 70593 74584: contig of 3993 bp in length
* 74585 74603: gap of unknown length
* 74604 79275: contig of 4672 bp in length
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* 121498 127118: contig of 5621 bp in length
* 127119 127137: gap of unknown length
* 127138 133999: contig of 6862 bp in length
* 134000 134018: gap of unknown length
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* 145556 145573: gap of unknown length
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* 165653 168077: contig of 2425 bp in length
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* 171253 Location/Qualifiers

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            /db_xref="taxon:9606"
            /clone="RP11-540P24"
BASE COUNT  47753 a 37720 c 36932 g 50252 t 900 others
ORIGIN

Query Match      53.6%; Score 869.4; DB 43; Length 173557;
Best Local Similarity 96.8%; Pred. No. 7.5e-142;
Matches 919; Conservative 0; Mismatches 26; Indels 4; Gaps 3;

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Db 51637 CCGGGAAGCTGTGTGAGAGTGTGGCGTGTGCGCTTGTCAGCGTGAGGCGCGGAGACCG 51696

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Db 51697 TGTGCT-GGCATGTGGGGAGAGAT-GGAGCCCGACCTTCAGCGATGTGCTATTTCCTGGA 51754

QY 794 CCGCGAGCCCGACAGGCTGAGAGCTTCAGGTCATCGAGACTCAGAGCCCGACCGCG 853
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QY 854 CCGGAGCTCAGAGCCCGCTCAGCTGCTCTTAAGCGTGACAAATCACAGGAGCGGACCG 913
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Db 51815 CCGGAGCTCAGAGCCCGCTCAGCTGCTCTTAAGCGTGACAAATCACAGGAGCGGACCG 51874

QY 914 CCGCTTCGGGGCCACATTGTCAGAGCCAGCTGAGCGCTGAGCGAGTGTGCTGCTGG 973
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Db 51875 CCGCTTCGGGGCCACATTGTCAGAGCCAGCTGAGCGCTGAGCGAGTGTGCTGCTGG 51934

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QY 914 CCGCTTCGGGGCCACATTGTCAGAGCCAGCTGAGCGCTGAGCGAGTGTGCTGCTGG 973
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QY 1034 CTACGCCCGGCTCACAAGAGTGGAGACTGTGTGTGAGAGATGTGTGGCATCTGCTT 1093
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Db 52053 CCGGGCGGTGGCTGAGACACCACTGGCTCAGTTGGCTCTTGCCCCCTAGACTCTTTTA 52112

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Db 52173 CTACCGCTGGGGCGTCTCTGTGTAGAGAGGAGCAGCTTCACACCCATGGGAGTGTCCGG 52232

QY 1274 GCGAGGAGCTGAAGAGACTCCAGCGCTGCTCTCTGGAACGTGCTACTGGGTCCAGAA 1333
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Db	52293	GCCTCTCAGCCAGAGGAGGAGCTGGCCCTTGGAAAGGAACTGAGCTGGGGGACACTGGCTTC	52352
QY	1394	TGCATCTCCTCTGCATGAAGATACACATTTGAGACTTGACTTGGGCAACACAGCTTC	1453
Db	52353	TGCCATCTCCTCTGCATGAAGATACACATTTGAGACTTGACTTGGGCAACACAGCTTC	52412
QY	1454	CCACACCCGCTGCTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGT	1513
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QY	1514	TGACCCCTCTCTCCCTAGAGACCTTGAAGCTGGCAAGGGGACCTCCCAACTCAGACCTGCTCT	1573
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REFERENCE Unclassified.  
1 (Pages 1 to 1056)  
AUTHORS Ingham, P.W., McMahon, A.P. and Tabin, C.J.  
TITLE Vertebrate embryonic pattern-inducing proteins and uses related thereto  
JOURNAL Patent: US 5789543-A 5 04-AUG-1998;  
FEATURES location/Qualifiers  
source 1. .1056

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Best Local Similarity	88.2%;	Pred. NO. 8.6e-137;		
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Db	61	AACACAGGGTGGCGACCGCTTATACCCAGCGCTGCAAGAGACGGTCTGAACCTGCTGCGCC	120
OY	396	ATTCGTGTGATGAACACAGTGGCCGGTGTGAAGCTGCGGGGTGACCCGAGGCTGGAGAG	455
Db	121	ATTCGTGTGATGAACACAGTGGCCGGTGTGAAGCTGCGGGGTGACCCGAGGCTGGAGAG	180
OY	456	GACGGCCACCACTAGAGAGATCCCTGATTATAGAGCGCGCGGGTGGACATTCACCACA	515
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OY	516	TCAGACCCGACCGCAATTAAGTATGACTGCTGGCGGCTTGACATGAGAGCGCGGCTT	575
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OY	636	GGCGACACCAAGACGGGGGGCTCTTCCTCGCGGAGGCCAGATGACGTGGAGAGTGG	695
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OY	696	GCGCGTGTGGCCTTGTTCAGCGCCGTGAGGCCGGGAGACCGTGTCTGTGCCATGGGGAGAT	755
Db	421	GAGGCTGTGGCCCTGTCAAGTGTAAAGCCAGGAGACCGGGTGTCTGGCATGGGGAGAT	480
OY	756	GGGAGCCCCACCTTCACGCGATGTCTCATTTTCCTGTGAGCCGGAGCCCCACAGCTGGA	815
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OY	876	CTGCTCTTATCGGCTGCATTCACACGAGACCGGCGCCGCTTCGGGGCACATTGTCC	935
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KEYWORDS	AR063082.1	GI:5990773			
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REFERENCE	Unknown.				
AUTHORS	Unclassified.				
TITLE	1 (bases 1 to 1056)				
JOURNAL	Ingham,P.W., McMahon,A.P. and Tabin,C.J.				
FEATURES	Vertebrate embryonic pattern-inducing proteins, and uses related thereto				
source	Patent: US 5844079-A 3 01-DEC-1998;				
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BASE COUNT	204 a	321 c	312 g	219 t	
ORIGIN					
Query Match	52.0%;	Score 843.2;	DB 5;	Length 1056;	

Best Local Similarity 88.2%; Pred. No. 8.6e-137;  
Matches 928; Conservative 0; Mismatches 123; Indels 1; Gaps 1;

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Db 1 GAGCGCTTAAAGAGGCTACCCCAATTAATCCAGACATCTCTTCAAGAGGAGAG 60
OY 336 AACACAGGCGCGACCGCTCATGACCCAGCGCTGCAAGAGACCGCTGAATCGTGCT 395
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Db 61 AACACAGGCGCGACCGCTCATGACCCAGCGCTGCAAGAGACCGCTGAATCGTGCT 120
OY 396 ATCTGCTGATGAACAGTGGCGCGCTGGAAGCTGGGCTGCGGAGGCTGCGAGAG 455
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Db 121 ATCTGCTGATGAACAGTGGCGCTGGAAGCTGGGCTGCGGAGGCTGCGAGAG 180
OY 456 GAGCGCCACACTAGAGAGAGTCCCTGATTAAGAGGCGCGCGCTGAGCATCACCACA 515
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Db 181 GATGGCCATCACTAGAGAGGAGTCTTAACATAGAGGCGCGCGCTGATATCACCACC 240
OY 516 TCAGACCGGCGGCAATAAGTATGAGACTGCTGGCGCTTGACAGTGAAGCGCGCTTT 575
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Db 241 TCAGACCGGCGGCAATAAGTATGAGACTGCTGGCGCTTGACAGTGAAGCGCGCTTC 300
OY 576 GACTGGGTATATACAGTCAAGGCCCAAGGCTGCTGCTCAAGTCCGAGCACTCG 635
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OY 636 GCGCGAGCCAGAGGCGCGCTGCTTCCCTGCGGAGCCGAGTACGCTGAGAGTGGG 695
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Db 361 GCGCGAGCCAGAGGCGCGCTGCTTCCCTGCGGAGCCGAGTGGCGCTGAGAGAGGG 420
OY 696 GCGCGGTGGCTTTCAGAGCGCTGAGGCGCGGAGACCGTGTGCTGGCCATGGGGAGAT 755
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OY 936 AGCCAGGTGAGCGCTGAGCATGAGTGTGCTGGGCTGGGAGGCGGCTGAGCGCTGCC 995
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OY 996 CCGGTGGAGCTTCTCTACACAGCTGGGCGCTGAGGCGCTGAGCGGCTGAGCGGCTG 1055
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Db 721 CCGGTGGAGCTTCTCTACACAGCTGGGCGCTGAGGCGCTGAGCGGCTGAGCGGCTG 780
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Db 1021 AACCACTGCCCTCTCTGGAAGTCTGTGGCTGG 1052

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RESULT 8
MIMH 1011 bp mRNA
LOCUS M.musculus (C57BL/6J) Ith mRNA.
DEFINITION X76291
ACCESSION X76291.1 GI:2440120
VERSION Ith gene; Indian hedgehog protein.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1011)
AUTHORS McMahon,A.P.
TITLE Submitted (24-NOV-1993) A.P. McMahon, Harvard University, 16
JOURNAL Divinity Ave., Cambridge, MA 02138, USA
REMARK 2 (bases 1 to 1011)
REFERENCE 2 (bases 1 to 1011)
AUTHORS Echelard,Y., Epstein,D.J., St-Jacques,B., Shen,L., Mohler,J.,
McMahon,J.A. and McMahon,A.P.
TITLE Sonic hedgehog, a member of a family of putative signaling
molecules, is implicated in the regulation of CNS polarity
JOURNAL Cell 75 (7), 1417-1430 (1993)
MEDLINE 94094334
REFERENCE 3 (bases 1 to 1011)
AUTHORS St-Jacques,B.
TITLE Direct Submission
JOURNAL Submitted (14-APR-1997) B. St-Jacques, Harvard University, 16
Divinity Ave., Cambridge, MA 02138, USA
REMARK 4 (bases 1 to 1011)
COMMENT revised by author 25-SEP-97
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Best Local Similarity 88.7%; Pred. No. 2.9e-134;
Matches 897; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
OY 276 GAGCGCTTAAAGAGGCTACCCCAATTAATCCAGACATCTCTTCAAGAGGAGAG 335
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Db 1 GAGCGCTTAAAGAGGCTACCCCAATTAATCCAGACATCTCTTCAAGAGGAGAGAG 60
OY 336 AACACAGGCGCGACCGCTCATGACCCAGCGCTGCAAGAGACCGCTGAATCGTGCT 395
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Db 61 AACACAGGCGCGACCGCTCATGACCCAGCGCTGCAAGAGACCGCTGAATCGTGCT 120

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[illegible]

TITLE		Direct Submission	
JOURNAL		Submitted (29-SEP-1998) to the DDBJ/EMBL/GenBank databases. Genshu Tate, Shoma University Fujigaoka Hospital, Department of Surgical Pathology, Fujigaoka 1-30, Aoda-ku, Yokohama, Kanagawa 227-8501, Japan (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632, Fax:81-45-972-6242)	
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QY	685 TGGAGATGGGGCGCGGTGCGCTTGTCAGCGGTAGCGCCGGAGACCGTGTCGGCCA	744	
Db	70 TGGAGATGGGGCGCGGTGCGCTTGTCAGCGGTAGCGCCGGAGACCGTGTCGGCCA	129	
QY	745 TGGGGAGATGGGAGCCCACTTCACGCATGTGCTCATTTTCTTGAACGGAGCCCC	804	
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QY	805 ACAGGCTAGAGCCTTCAGGTCATCGAGTCACAGAGACCCCAAGCGGCGTGGAGTCA	864	
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QY	865 CACCGCTACCTGCTCTTACGGCTGACCAATCACACGAGAGCGGACCGCGTTCCGGG	924	
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QY	925 CCAATTGGCCAGCAGCTGCAAGCTGGCCAGTACGTGCTGGTGGCTGGGGTGCAGGCC	984	
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Db	490 CTGACCACTACCTGGCTAGTTGGCTTCGGCCCTTGAAGCTCTTTCACAGCTTGGGAT	549	
QY	1165 GGGGCACTGGAACCCGGGGGAGGGGTGTGCATGTGTACCCCAAGTGTGCTTACCGCTTGG	1224	

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Db 610 GGGCTCTCTCTAGTAAGAGGAGGAGCTTCCACCCAGCTGGGATGTCGGGGAGGAGCT 669  
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LOCUS Notophthalmus viridescens hedgehog segment polarity homolog mRNA,  
DEFINITION complete cds.  
ACCESSION AF047466.1 GI:2896034  
VERSION AF047466.1 GI:2896034  
KEYWORDS eastern newt,  
ORGANISM Notophthalmus viridescens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.  
REFERENCE 1 (bases 1 to 1635)  
AUTHORS Stark,D.R., Gates,P.B., Brookes,J.P. and Ferretti,P.  
TITLE Hedgehog homologue from Notophthalmus viridescens  
JOURNALS Dev. Dyn. (1998) In press  
REFERENCE 2 (bases 1 to 1635)  
AUTHORS Stark,D.R., Gates,P.B., Brookes,J.P. and Ferretti,P.  
TITLE Direct Submission  
JOURNALS Submitted (05-FEB-1998) MMB, The Krebs Institute, Western Bank,  
Sheffield S10 2TN, UK  
FEATURES  
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Query Match 38.2%; Score 618.8; DB 4; Length 1635;  
Best Local Similarity 70.3%; Pred. No. 4.9e-98;  
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OY 365 GCGCTCAAGAGAGCGCTGATCGCTATCTCGGTGATGAACAGTGGCCGGTGT 424  
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OY 425 GAAGCTGGGGTGAACCGAGGGCTGGAGAGAGAGCGCCACCTCAGAGAGTCCCTGA 484  
Db 363 CAACCTGGGGTGAACCGAGGGCTGGAGAGAGAGCGCCACCTCAGAGAGTCCCTGA 422  
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RESULT	12
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DEFINITION	Xenopus laevis banded hedgehog protein mRNA, complete cds.
ACCESSION	U26404
VERSION	U26404.1 GI:1147831
KEYWORDS	.
SOURCE	African clawed frog. Xenopus laevis
ORGANISM	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE	1 (bases 1 to 1230) Ekker,S.C., McGrew,L.L., Lai,C.J., Lee,J.J., von Kessler,D.P., Moon,R.T. and Beachy,P.A. Distinct expression and shared activities of members of the hedgehog gene family of Xenopus laevis Development 121 (8), 2337-2347 (1995)
JOURNAL	95401852
MEDLINE	2 (bases 1 to 1230) Ekker,S.C., McGrew,L.L., Lai,C.-J., Lee,J.J., von Kessler,D.P., Moon,R.T. and Beachy,P.A. Direct Submission Submitted (05-MAY-1995) Stephen C. Ekker, Molecular Biology and Genetics, Johns Hopkins University, 725 N. Wolfe St, 714 PCMB, Baltimore, MD 21205, USA
AUTHORS	Baltimore, MD 21205, USA
TITLE	Location/Qualifiers
JOURNAL	1..1230 /organism="Xenopus laevis" /db_xref="taxon:8355"
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OY	644	CANAGACGGGGCGCTGCTCCCTCTGCGAGACCCAGGTATAGCCTGGAGAGATGGGGCGCTGT	703
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OY	704	GGCCTTTCAGCCGTGAGGCGGGGAGACCGTGTGCTGGCCATGGGGAGATGGGAGGCC	763
Db	639	ACCGATTTCACACTGAGGCCACAGCCCTAAGTGTCTCTGGCTATGGACAACAGTGGAGAGGCC	698
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Db	759	GGTTATTAAGACTCAGAGCCACACACCGTGTGTTGTCTTAAACACAGCCATTGTGATCTT	818
OY	884	TACGGCTGACATTCACACGGAAGCGGACCGCGCTTCCGGGCCACATTTGCGACGCCAGT	943
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Db	1059	AATATGTTAATATGGCTCTCTCCGGGTACTCTACAAATTAGAGTAATATAGAGGAACGCAACC	1118
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RESULT	13		
CHK2PAMED			
LOCUS	CHK2PAMED	1567 bp	mRNA
DEFINITION	Gallus gallus sonic hedgehog mRNA, complete cds.		
ACCESSION	U28099		
VERSION	U28099.1		
KEYWORDS			
SOURCE	chicken.		
ORGANISM	Gallus gallus		
REFERENCE	1 (bases 1 to 1567)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria		
	Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus		



AUTHORS Riddle,R.D., Johnson,R.L., Laufer,E. and Tablin,C.  
 TITLE Sonic hedgehog mediates the polarizing activity of the ZPA  
 JOURNAL Cell 75, 1401-1416 (1993)  
 MEDLINE 94094333  
 FEATURES  
 source Location/Qualifiers

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BASE COUNT 347 a 457 c 475 g 288 t  
 ORIGIN

Query Match 28.4%; Score 461.4; DB 4; Length 1567;  
 Best Local Similarity 65.2%; Pred. No. 8.1e-71;  
 Matches 766; Conservative 0; Mismatches 361; Indels 48; Gaps 4;

OY 163 GCGGACCGCGCAAACTGTCGCGCTGCTACAGAGTTCAGCCCAATGTGCGG 222  
 DB 333 GGAGGACCGCGCAAAAGCTGACCCGCTTACCTATAGAGTTATTCCTCAATGTGCGAG 392  
 OY 223 AGAAGACCTGGCGCGCGAGCGGAGCTATGAGGCAAGTCCCTGCGAGCTCCGAGCGT 282  
 DB 393 AGAAGACCTGAGGCGCGAGTGAAGATGAGAGGAGTCAAGAAATCCGAGAGAT 452  
 OY 283 TCAGAGAGCTCAACCCCAATTCAGATCATCTTCAAGGAGGAGAGAACAGAG 342  
 DB 453 TTAAGAGACTAATCCCAATTCAGATCATCTTCAAGGAGGAGAGAACAGAG 512  
 OY 343 GCGGACCGCGCTGATGACCGAGCGCTGCAAGAGCGCGCTGCACTGCTATCTCGG 402  
 DB 513 GAGCTGACAGATGATGACTGACCGCTGCAAGAGCAAGCTGATGCGCTGGGATCTCGG 572  
 OY 403 TGATGAACAGTGGCGCGGCTGGAAGCTGCGGCTGACCGAGGCTGGGACGAGAGCGCC 462  
 DB 573 TGATGAACAGTGGCGCGGCTGGAAGCTGCGGCTGACCGAGGCTGGGACGAGAGTGGCC 632  
 OY 463 ACCACTCAGAGAGTCCCTGATTAAGAGGCGCGGCTGGAGTCAATCAGCATCATGAGACC 522  
 DB 633 ATCACTCGAGAGATCGCTGCTAGAGAGTGGCGGCTGGAGTCAATCAGCATCATGAGATC 692  
 OY 523 GCGACCGCAATAGTATGAGTGTGCGCGCTTGGCAGTGAAGCGCGGCTTGTGACTGGG 582  
 DB 693 GCGACCGCAATAGTATGAGTGTGCGCGCTTGGCAGTGAAGCGCGGCTTGTGACTGGG 752  
 OY 583 TGATTAAGAGTCAAGAGCGCGGCTGATGCTGCTCAAGTCCAGAGCACTGGCGCGAG 642  
 DB 753 TGTACTAGAGTCAAGAGCGCGGCTGATGCTGCTCAAGAGCACTGGCGCGAG 812  
 OY 643 CCAGAGAGCGCGGCTGCTGCTGCGGAGCCAGGTACGCTGAGAGTGGGCGCGCTGG 702  
 DB 813 CGAAATCAAGAGAGTGGCTTCCCTGGCTCAGCCAGTGAAGTGAAGTGAAGAGGAGCA 872  
 OY 703 TGGCCTTGTGACCGGTGAGGCGGAGAGACCTGTGTGCGCATGGGAGAGATGGAGCC 762  
 DB 873 ACCTGGTGAAGAGCTGAGCCCTGGGAGCGGCTGTGCTGTGACGCGGAGCGCGCGC 932  
 OY 763 CCACCTTGAGGATGTGCTATTTCTGAGCGGAGCCCAAGGCTGAGAGCGCTTCC 822

DB 933 TGGCTACAGTACTTCTCTACCTTCTGACCGGATGAGACGCTCCGAAAGCTTCT 992  
 OY 823 AGGTATGAGAGACTGAGGACCGCCCGGAGCGGCTGAGCATGACACCGGCTGCTGT 882  
 DB 993 AGGTATGAGAGACTGAGGACCGCCCGGAGCGGCTGAGCATGACACCGGCTGCTGT 1052  
 OY 883 TTACGCTGACATGACAGGAGCGG-----CAGCCCGCTTCCGGGCGACAT 930  
 DB 1053 TTGTCGCGCGCGGAGCAACAGTGGAGGCGACAGGAGTCCAGTGGCCAGGCGCTCT 1112  
 OY 931 TTGCGAGCGAGTGAAGCTGCGCAAGCTGTATGTCTGTGGCGAGCGGCGAGCAAGC 1172  
 DB 1113 TCGCCAGCAACCTGAAGCTGCGCAAGCTGTATGTCTGTGGCGAGCGGCGAGCAAGC 1172  
 OY 985 TGCACCTGCGCGCGGAGGAGTGTCTGTACAC---ACGTGGCGCTCGGGGCGAGCGCC 1041  
 DB 1173 TGTCTGCGCGCGCTCTTCCAGACGCTCTATTCGCGGAGAGAGCGCTCGAGCGCTC 1232  
 OY 1042 CGCTCACAAGAGTGGAGACACTGTGTGAGAGATGTGTGATCTGCTTCCGCGCGCG 1101  
 DB 1233 CACTCAGCGCGCGGAGCAGCATCTCATCAACCGGAGTGTGGCTCTGCTACGCGCTCA 1292  
 OY 1102 TGGCTGACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161  
 DB 1293 TCGAGGAGCAGTGTGGGCGCATTTGGCGCTTGCACACATTCGCTTGGCTCAGGCGCTGC 1352  
 OY 1162 CATGGGCGAGCTGAGACCGCGGCGGAG-----GGTGTGC 1194  
 DB 1353 TGGCGCGCGCTGCGCGAGTGGGCGCATTCCTACTGCGCGCACACACACTGCGATCC 1412  
 OY 1195 ATGTGTACCCAGTGTCTTACCGCTGCGGCGCTGCTCTGCTAGAGAGGCGAGCTTCC 1254  
 DB 1413 ATGTGTACCGAGTGTCTTACCGCTGCGGCGCTGCTCTGCTAGAGAGGCGAGCTTCC 1472  
 OY 1255 ACCCACTGGGCTGTCCGGGCGAGGAGCTGAAG 1289  
 DB 1473 ATCCGCTGGCATGTGTGCGACCGCGGAGCTGAGAG 1507

## RESULT 14

LOCUS AR021198 1277 bp DNA PAT 05-DEC-1998  
 DEFINITION Sequence 1 from patent US 5789543.  
 ACCESSION AR021198  
 VERSION AR021198.1 GI:3975813  
 KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.  
 UNCLASIFIED.  
 REFERENCE 1 (bases 1 to 1277)  
 AUTHORS Ingham,P.W., McMahon,A.P. and Tablin,C.J.  
 TITLE Vertebrate embryonic pattern-inducing proteins and uses related  
 thereto US 5789543-A 1 04-AUG-1998;

JOURNAL Patent: US 5789543-A 1 04-AUG-1998;  
 FEATURES Location/Qualifiers  
 source 1.1277

BASE COUNT 262 a 396 c 387 g 232 t  
 ORIGIN

Query Match 28.3%; Score 459; DB 5; Length 1277;  
 Best Local Similarity 65.2%; Pred. No. 2.2e-70;  
 Matches 763; Conservative 0; Mismatches 360; Indels 48; Gaps 4;

OY 163 GCGGACCGCGCAAACTGTCGCGCTGCTACAGAGTTCAGCCCAATGTGCGG 222  
 DB 107 GGAGGACCGCGCAAAAGCTGACCCGCTTACCTATAGCAGTTATTCCTCAATGTGCGAG 166  
 OY 223 AGAAGACCTGGGCGCGAGCGCTATGAGGCAAGTGTGCTGCGAGCTCGAGCGCT 282  
 DB 167 AGAAGACCTGAGGCGCGAGTGAAGATATGAGGAGAGTTCACAAGAACTCCGAGAGAT 226







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